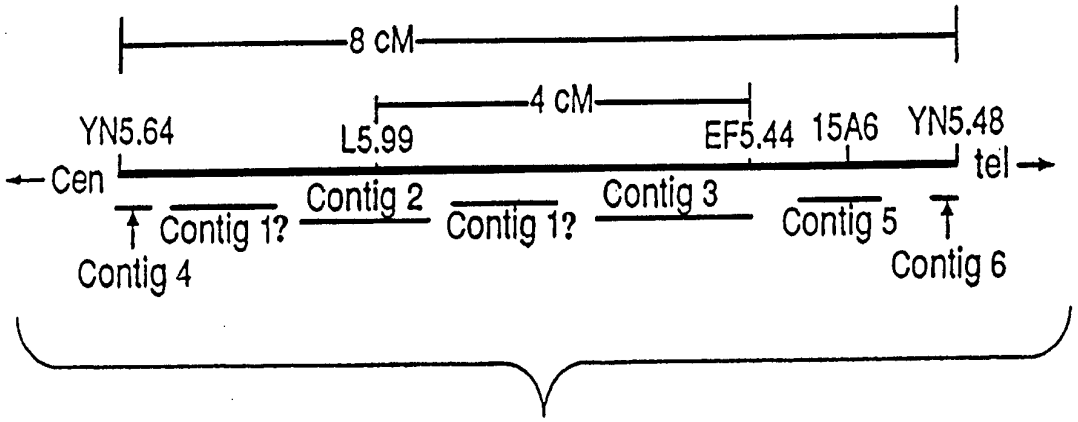

FIG. 1A

FIG. 1B-1

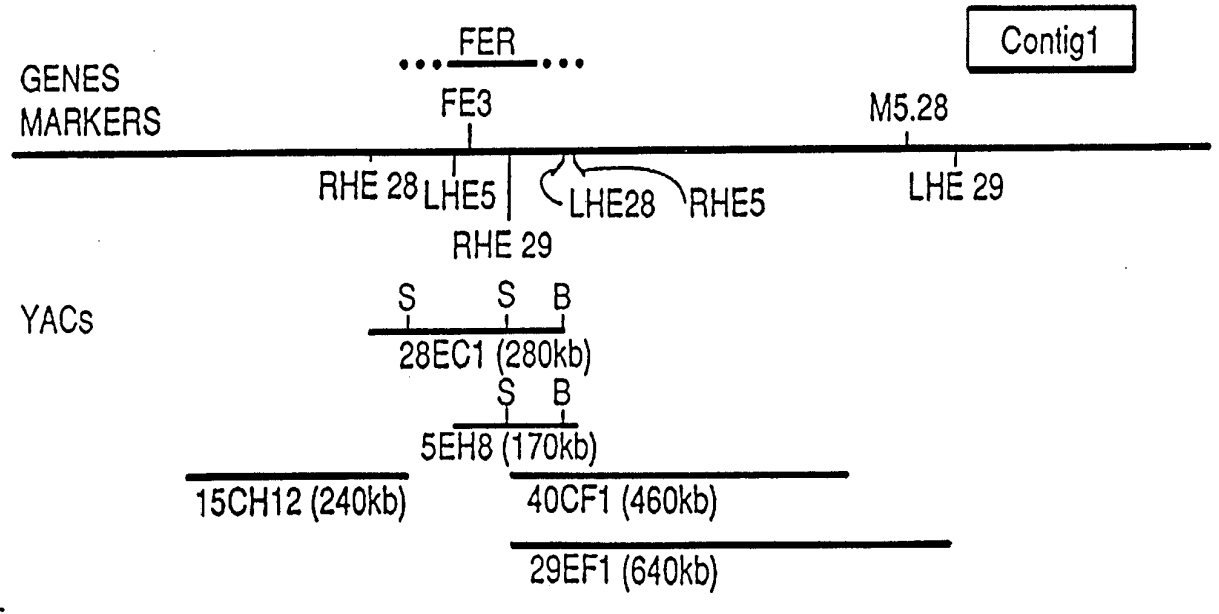

FIG. 1B-2

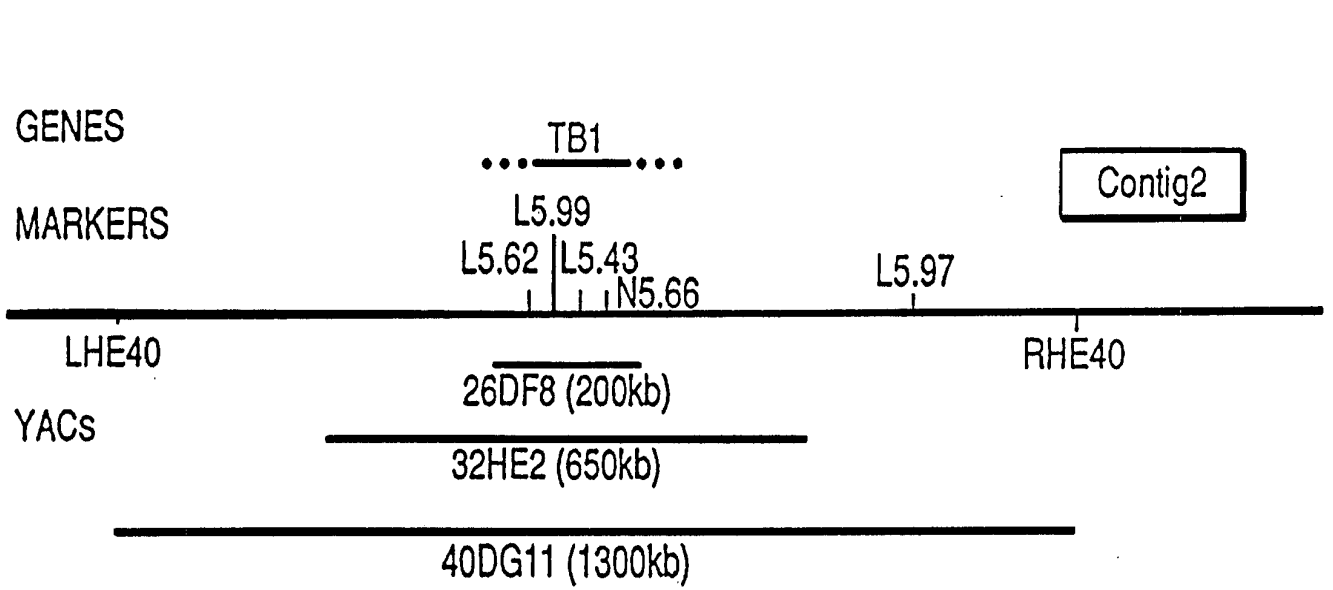

FIG. 1B-3

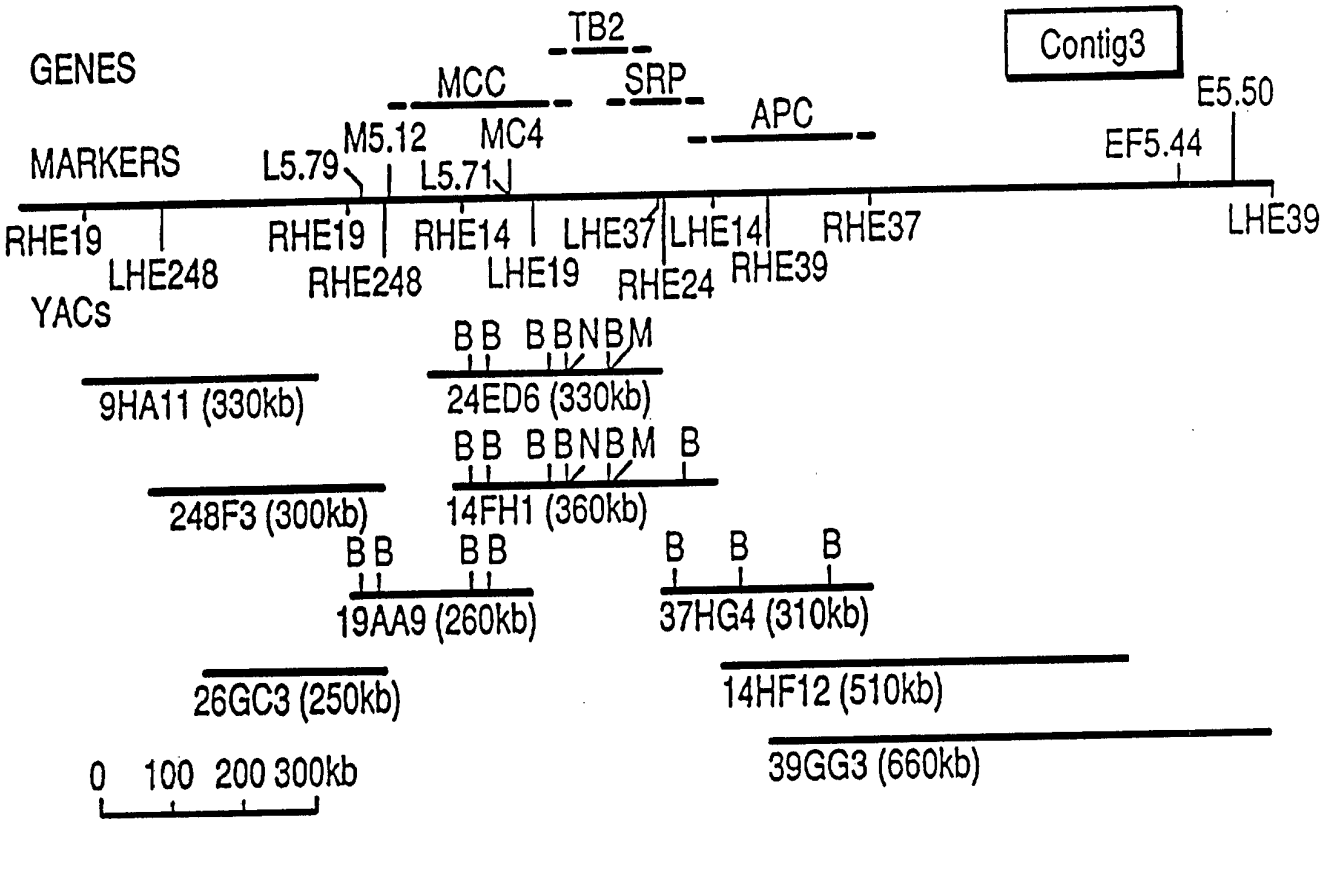

FIG. 2A

TB1 Amino Acid Sequence

VAPVVVGSGR APRHPAPAAM HPRRPDGFDG LGYRGGARDE QGFGGAFPAR SFSTGSDLGH 60

WVTTPPDIPG SRNLHWGEKS PPYGVPTTST PYEGPTEEPF SSGGGGSVQG QSSEQLNRFA 120

GFGIGLASLF TENVLAHPCI VLRRQCQVNY HAQHYHLTPF TVINIMYSFN KTQGPRALWK 180

GMGSTFIVQG VTLGAEGIIS EFTPLPREVL HKWSPKQIGE HLLLKSLTYV VAMPFYSASL 240

IETVQSEIIR DNTGILECVK EGIGRVIGMG VPHSKRLLPL LSLIFPTVLH GVLHYIISSV 300

IQKFVLLILK RKTYNSHLAE STSPVQSMLD AYFPELIANF AASLCSDVIL YPLETVLHRL 360

HIQGTRTIID NTDLGYEVLP INTQYEGMRD CINTIRQEEG VFGFYKGFGA VIIQYTLHAA 420

VLQITKIIYS TLLQ 434

FIG. 2B

TB2 Amino Acid Sequence

ELRRFDRFLH EKNCMTDLLA KLEAKTGVNR SFIALGVIGL VALYLVFGYG ASLLCNLIGF 60

GYPAYISIKA IESPNKEDDT QWLTYWVVYG VFSIAEFFSD IFLSWFPFYY ILKCGFLLWC 120

MAPSPSNGAE LLYKRIIRPF FLKHESQMDS VVKDLKDKAK ETADAITKEA KKATVNLLGE 180

EKKST 185

FIG. 3A

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu
1 5 10 15

Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn
20 25 30

His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu
35 40 45

Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly
50 55 60

Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser
65 70 75 80

Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr
85 90 95

Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro
100 105 110

FIG. 3B

```
Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg
        115                 120                 125

Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu
    130                 135                 140

Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala
145                 150                 155                 160

Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu
                165                 170                 175

Asn Phe Ser Leu Gln Thr Asp Leu Thr Arg Arg Gln Leu Glu Tyr Glu
            180                 185                 190

Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln
        195                 200                 205

Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile
    210                 215                 220
```

FIG. 3C

```
Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr
225                 230                 235                 240

Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp
                245                 250                 255

Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala
            260                 265                 270

Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr
        275                 280                 285

Ala Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu
    290                 295                 300

Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser
305                 310                 315                 320

Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala
                325                 330                 335
```

FIG. 3D

```
Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys
            340                 345                 350

Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val
        355                 360                 365

Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser
    370                 375                 380

Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly
385                 390                 395                 400

Arg Arg Glu Ile Arg Val Leu His Leu Leu Glu Gln Ile Arg Ala Tyr
                405                 410                 415

Cys Glu Thr Cys Trp Glu Trp Gln Glu Ala His Glu Pro Gly Met Asp
            420                 425                 430

Gln Asp Lys Asn Pro Met Pro Ala Pro Val Glu His Gln Ile Cys Pro
        435                 440                 445
```

FIG. 3E

```
Ala Val Cys Val Leu Met Lys Leu Ser Phe Asp Glu Glu His Arg His
    450                 455                 460

Ala Met Asn Glu Leu Gly Gly Leu Gln Ala Ile Ala Glu Leu Leu Gln
465                 470                 475                 480

Val Asp Cys Glu Met Tyr Gly Leu Thr Asn Asp His Tyr Ser Ile Thr
                485                 490                 495

Leu Arg Arg Tyr Ala Gly Met Ala Leu Thr Asn Leu Thr Phe Gly Asp
            500                 505                 510

Val Ala Asn Lys Ala Thr Leu Cys Ser Met Lys Gly Cys Met Arg Ala
        515                 520                 525

Leu Val Ala Gln Leu Lys Ser Glu Ser Glu Asp Leu Gln Gln Val Ile
    530                 535                 540

Ala Ser Val Leu Arg Asn Leu Ser Trp Arg Ala Asp Val Asn Ser Lys
545                 550                 555                 560
```

FIG. 3F

Lys Thr Leu Arg Glu Val Gly Ser Val Lys Ala Leu Met Glu Cys Ala
565 570 575

Leu Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu
580 585 590

Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala
595 600 605

Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser
610 615 620

Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg
625 630 635 640

Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu
645 650 655

Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His
660 665 670

FIG. 3G

Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser
675 680 685

Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val
690 695 700

Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met
705 710 715 720

Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys
725 730 735

Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu
740 745 750

His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His
755 760 765

Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser
770 775 780

FIG. 3H

```
His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val
785                 790                 795                 800

Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr
                805                 810                 815

Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro
            820                 825                 830

Ser Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys
        835                 840                 845

Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His
    850                 855                 860

Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile
865                 870                 875                 880

Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala
                885                 890                 895
```

FIG. 3I

```
Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu
            900                 905                 910

His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala
        915                 920                 925

His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn
    930                 935                 940

Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser
945                 950                 955                 960

Asn Asp Ser Leu Asn Ser Val Ser Ser Asn Asp Gly Tyr Gly Lys Arg
                965                 970                 975

Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser
            980                 985                 990

Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile
        995                 1000                1005
```

FIG. 3J

```
His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro
    1010                1015                1020

Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg
1025                1030                1035                1040

Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile
                1045                1050                1055

Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser
            1060                1065                1070

Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys
        1075                1080                1085

Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser
    1090                1095                1100

Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly
1105                1110                1115                1120
```

FIG. 3K

Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu
1125 1130 1135

Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln
1140 1145 1150

His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu
1155 1160 1165

Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala
1170 1175 1180

Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser
1185 1190 1195 1200

Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu
1205 1210 1215

Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His
1220 1225 1230

FIG. 3L

Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr
1235 1240 1245

Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val
1250 1255 1260

Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu
1265 1270 1275 1280

Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala
1285 1290 1295

Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Gly Lys Ile Gly
1300 1305 1310

Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln
1315 1320 1325

His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser
1330 1335 1340

FIG. 3M

```
Glu Ser Ala Arg His Lys Ala Val Glu Phe Pro Ser Gly Ala Lys Ser
1345                1350                1355                1360

Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr
                1365                1370                1375

Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser
            1380                1385                1390

Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu
        1395                1400                1405

Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro
    1410                1415                1420

Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro
1425                1430                1435                1440

Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys
                1445                1450                1455
```

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FIG. 3N

Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val
1460 1465 1470

Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu
1475 1480 1485

Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser
1490 1495 1500

Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val
1505 1510 1515 1520

Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu
1525 1530 1535

Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu
1540 1545 1550

Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp
1555 1560 1565

FIG. 30

Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro
1570 1575 1580

Thr Lys Ser Ser Arg Lys Gly Lys Lys Pro Ala Gln Thr Ala Ser Lys
1585 1590 1595 1600

Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys
1605 1610 1615

Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe
1620 1625 1630

Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro
1635 1640 1645

Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser
1650 1655 1660

Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln
1665 1670 1675 1680

FIG. 3P

Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser
1685 1690 1695

Thr Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu
1700 1705 1710

Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile
1715 1720 1725

Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys
1730 1735 1740

Lys Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro
1745 1750 1755 1760

Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Lys Pro Thr Ser Pro Val
1765 1770 1775

Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn
1780 1785 1790

FIG. 3Q

Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn
1795 1800 1805

Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn
1810 1815 1820

Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe
1825 1830 1835 1840

Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe
1845 1850 1855

Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Asp Val
1860 1865 1870

Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys
1875 1880 1885

Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln
1890 1895 1900

FIG. 3R

Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg
1905 1910 1915 1920

Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser
1925 1930 1935

Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln
1940 1945 1950

Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser
1955 1960 1965

Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn
1970 1975 1980

Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser
1985 1990 1995 2000

Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp
2005 2010 2015

FIG. 3S

Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile
2020 2025 2030

Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro
2035 2040 2045

Lys Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser
2050 2055 2060

Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu
2065 2070 2075 2080

Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser
2085 2090 2095

Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val
2100 2105 2110

Ser Ser Leu His Gln Ala Ala Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala
2115 2120 2125

FIG. 3T

Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu
2130 2135 2140

Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr
2145 2150 2155 2160

Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu
2165 2170 2175

Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys
2180 2185 2190

Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu
2195 2200 2205

Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile
2210 2215 2220

Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser
2225 2230 2235 2240

FIG. 3U

Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro
2245 2250 2255

Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg
2260 2265 2270

Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln
2275 2280 2285

Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser
2290 2295 2300

Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro
2305 2310 2315 2320

Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile
2325 2330 2335

Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser
2340 2345 2350

FIG. 3V

Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser
2355 2360 2365

Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu
2370 2375 2380

Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly
2385 2390 2395 2400

Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu
2405 2410 2415

Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser
2420 2425 2430

Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro
2435 2440 2445

Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser
2450 2455 2460

FIG. 3W

Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln
2465 2470 2475 2480

Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His
2485 2490 2495

Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser
2500 2505 2510

Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile
2515 2520 2525

Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser
2530 2535 2540

Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg
2545 2550 2555 2560

Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala
2565 2570 2575

FIG. 3X

Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val
2580 2585 2590

Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala
2595 2600 2605

Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn
2610 2615 2620

Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser
2625 2630 2635 2640

Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp
2645 2650 2655

Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly
2660 2665 2670

Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu
2675 2680 2685

FIG. 3Y

```
Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln
    2690                2695                2700

Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn
2705                2710                2715                2720

Arg Leu Thr Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr
                2725                2730                2735

Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn
            2740                2745                2750

Glu Ser Pro Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Ser
        2755                2760                2765

Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe
    2770                2775                2780

Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala
2785                2790                2795                2800
```

FIG. 3Z

Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg
2805 2810 2815

Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys
2820 2825 2830

Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val
2835 2840

FIG. 4A

```
APC      203  LGTCQDMEKRAQRRIARIQQIEKDILRIRQL  233
              |     :: || ||||||:|    |     |
RAL2     576  LTGAKGLQLRALRRIARIEQGGTAISPTSPL  606
```

FIG. 4B

```
APC      453  MKLSFDEEHRHAMNELGGLQAIAELLQVD  481
              :     |  :  ||:|||| :   : :
M3 MACHR 249  LYWRIYKETEKRTKELAGLQASGTEAETE  277
              ||  :  |  :  ||||||
MCC      220  LYPNLAEERSRWEKELAGLREENESLTAM  248
              :     ||: :  ||:||    | |
APC      453  MKLSFDEEHRHAMNELGGLQAIAELLQVD  481
```

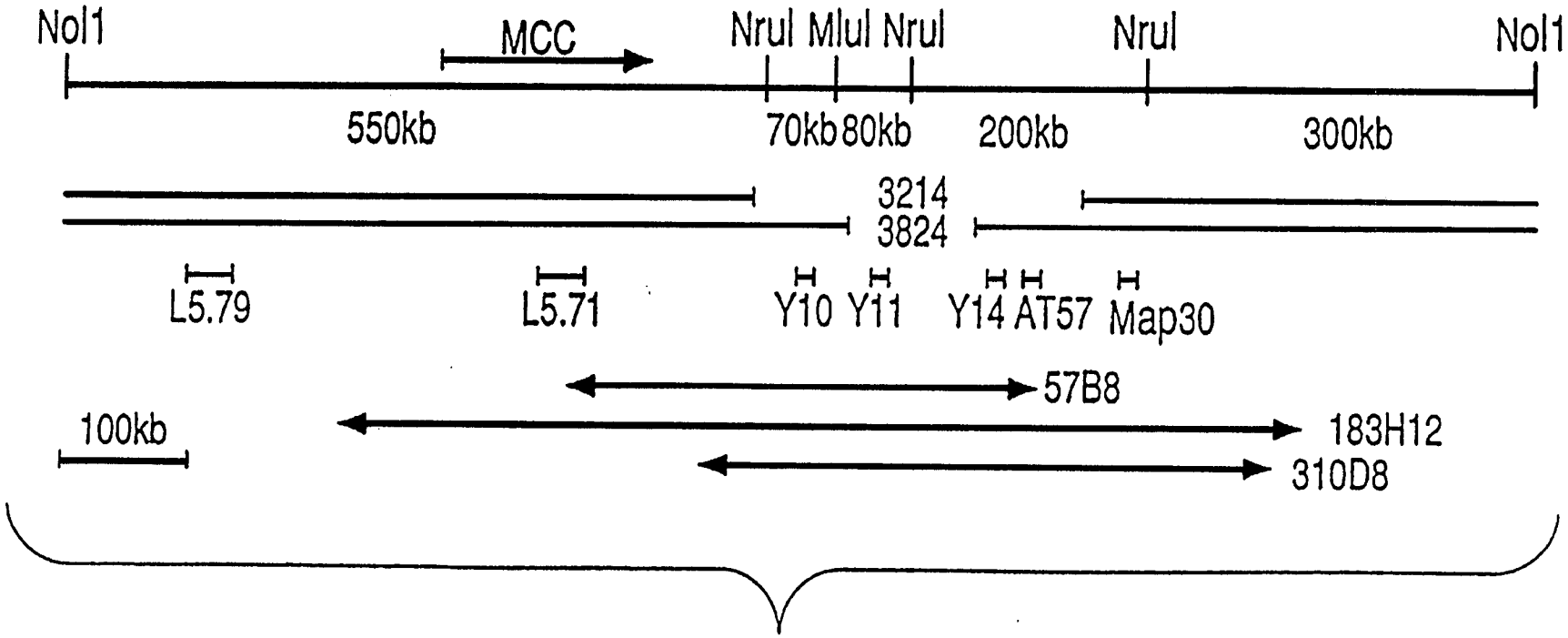

FIG. 5

FIG. 6A

```
                                                28                                                  55
GCA GTC GCC GCT CCA GTC TAT CCG GCA CTA GGA ACA GCC CCG GGN GGC GAG ACG
Ala Val Ala Ala Pro Val Tyr Pro Ala Leu Gly Thr Ala Pro Gly Gly Glu Thr
                                                82                                                 109
GTC CCC GCC ATG TCT GCG GCC ATG AGG GAG AGG TTC GAC CGG TTC CTG CAC GAG
Val Pro Ala MET Ser Ala Ala MET Arg Glu Arg Phe Asp Arg Phe Leu His Glu
                                               136                                                 163
AAG AAC TGC ATG ACT GAC CTT CTG GCC AAG CTC GAG GCC AAA ACC GGC GTG AAC
Lys Asn Cys MET Thr Asp Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn
                                               190                                                 217
AGG AGC TTC ATC GCT CTT GGT GTC ATC GGA CTG GTG GCC TTG TAC CTG GTG TTC
Arg Ser Phe Ile Ala Leu Gly Val Ile Gly Leu Val Ala Leu Tyr Leu Val Phe
                                               244                                                 271
GGT TAT GGA GCC TCT CTC CTC TGC AAC CTG ATA GGA TTT GGC TAC CCA GCC TAC
Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Gly Tyr Pro Ala Tyr
                                               298                                                 325
ATC TCA ATT AAA GCT ATA GAG AGT CCC AAC AAA GAA GAT GAT ACC CAG TGG CTG
Ile Ser Ile Lys Ala Ile Glu Ser Pro Asn Lys Glu Asp Asp Thr Gln Trp Leu
                                               352                                                 379
ACC TAC TGG GTA GTG TAT GGT GTG TTC AGC ATT GCT GAA TTC TTC TCT GAT ATC
Thr Tyr Trp Val Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile
                                               406                                                 433
TTC CTG TCA TGG TTC CCC TTC TAC TAC ATG CTG AAG TGT GGC TTC CTG TTG TGG
Phe Leu Ser Trp Phe Pro Phe Tyr Tyr MET Leu Lys Cys Gly Phe Leu Leu Trp
                                               460                                                 487
TGC ATG GCC CCG AGC CCT TCT AAT GGG GCT GAA CTG CTC TAC AAG CGC ATC ATC
Cys MET Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg Ile Ile
                                               514                                                 541
CGT CCT TTC TTC CTG AAG CAC GAG TCC CAG ATG GAC AGT GTG GTC AAG GAC CTT
Arg Pro Phe Phe Leu Lys His Glu Ser Gln MET Asp Ser Val Val Lys Asp Leu
```

FIG. 6B

```
                                    568                                 595
AAA GAC AAG TCC AAA GAG ACT GCA GAT GCC ATC ACT AAA GAA GCG AAG AAA GCT
Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr Lys Glu Ala Lys Lys Ala
                                    622
ACC GTG AAT TTA CTG GGT GAA GAA AAG AAG AGC ACC TAA ACC AGA
Thr Val Asn Leu Leu Gly Glu Glu Lys Lys Ser Thr
        640         650         660         670         680         690         700
 CTAAACCAGA CTGGATGGAA ACTTCCTGCC CTCTCTGTAC CTTCCTACTG GAGCTTGATG TTATATTAGG
        710         720         730         740         750         760         770
 GACTGTGGTA TAATTATTTT AATAATGTTG CCTTGGAAAC ATTTTTGAGA TATTAAAGAT TGGAATGTGT

        780         790         800         810         820         830         840
 TGTAAGTTTC TTTGCTTACT TTTACTGTCT ATATATATAG GGAGCACTTT AAACTTAATG CAGTGGGCAG
        850         860         870         880         890         900         910
 TGTCCACGTT TTTGGAAAAT GTATTTTGCC TCTGGGTAGG AAAAGATGTA TGTTGCTATC CTGCAGGAAA
        920         930         940         950         960         970         980
 TATAAACTTA AAATAAAATT ATATACCCCA CAGGCTGTGT ACTTTACTGG GCTCTCCCTG CACGSATTTT
        990        1000        1010        1020        1030        1040        1050
 CTCTGTAGTT ACATTTAGGR TAATCTTTAT GGTTCTACTT CCTRTAATGT ACAATTTTAT ATAATTCNGR
       1060        1070        1080        1090        1100        1110        1120
 AATGTTTTTA ATGTATTTGT GCACATGTAC ATATGGAAAT GTTACTGTCT GACTACANCA TGCATCATGC
       1130        1140        1150        1160        1170        1180        1190
 TCATGGGGAG GGAGCAGGGG AAGGTTGTAT GTGTCATTTA TAACTTCTGT ACAGTAAGAC CACCTGCCAA
       1200        1210        1220        1230        1240        1250        1260
 AAGCTGGAGG AACCATTGTG CTGGTGTGGT CTACTAAATA ATACTTTAGG AAATACGTGA TTAATATGCA
       1270        1280        1290        1300        1310        1320        1330
 AGTGAACAAA GTGAGAAATG AAATCGAATG GAGATTGGCC TGGTTGTTTC CGTAGTATAT GGCATATGAA
       1340        1350        1360        1370        1380        1390        1400
```

FIG. 6C

TACCAGGATA GCTTTATAAA GCAGTTAGTT AGTTAGTTAC TCACTCTAGT GATAAATCGG GAAATTTACA
1410 1420 1430 1440 1450 1460 1470
CACACACACA CACACACACA CACACACACA CACACACACA CACACACACA GAGTACCCTG TAACTCTCAA
1480 1490 1500 1510 1520 1530 1540
TTCCCTGAAA AACTAGTAAT ACTGTCTTAT CTGCTATAAA CTTTACATAT TTGTCTATTG TCAAGATGCT
1550 1560 1570 1580 1590 1600 1610
ACANTGGAMN CCATTTCTGG TTTTATCTTC ANAGSGGAGA NACATGTTGA TTTAGTCTTC TTTCCCAATC
1620 1630 1640 1650 1660 1670 1680
TTCTTTTTTA AMCCAGTTTN AGGMNCTTCT GRAGATTTGY CCACCTCTGA TTACATGTAT GTTCTYGTTT
1690 1700 1710 1720 1730 1740 1750
GTATCATKAG CAACAACATG CTAATGRCGA CACCTAGCTC TRAGMGCAAT TCTGGGAGAN TGARAGGNWG
1760 1770 1780 1790 1800 1810 1820
TATARAGTMN CCCATAATCT GCTTGGCAAT AGTTAAGTCA ATCTATCTTC AGTTTTTCTC TGGCCTTTAA
1830 1840 1850 1860 1870 1880 1890
GGTCAAACAC AAGAGGCTTC CCTAGTTTAC AAGTCAGAGT CACTTGTAGT CCATTTAAAT GCCCTCATCC
1900 1910 1920 1930 1940 1950 1960
GTATTCTTTG TGTTGATAAG CTGCACAKGA CTACATAGTA AGTACAGANC AGTAAAGTTA ANNCGGATGT
1970 1980 1990 2000 2010 2020 2030
CTCCATTGAT CTGCGAANTC GNTATAGAGA GCAATTTGTC TGGACTAGAA AATCTGAGTT TTACACCATA
2040 2050 2060 2070 2080 2090 2100
CTGTTAAGAG TCCTTTTGAA TTAAACTAGA CTAAAACAAG TGTATAACTA AACTAACAAG ATTAAATATC
2110 2120 2130 2140 2150 2160 2170
CAGCCAGTAC AGTATTTTTT AAGGCAAATA AAGATGATTA GCTCACCTTG AGNTAACAAT CAGGTAAGAT

2180 2190 2200 2210 2220 2230 2240
CATNACAATG TCTCATGATG TNAANAATAT TAAAGATATC AATACTAAGT GACAGTATCA CNNCTAATAT

FIG. 6D

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      2250        2260        2270        2280        2290        2300        2310
AATATGGATC AGAGCATTTA TTTTGGGGAG GAAAACAGTG GTGATTACCG GCATTTTATT AAACTTAAAA
      2320        2330        2340        2350        2360        2370        2380
CTTTGTAGAA AGCAAACAAA ATTGTTCTTG GGAGAAAATC AACTTTTAGA TTAAAAAAAT TTTAAGTAWC
      2390        2400        2410        2420        2430        2440        2450
TAGGAGTATT TAAATCCTTT TCCCATAAAT AAAAGTACAG TTTTCTTGGT GGCAGAATGA AAATCAGCAA
      2460        2470        2480        2490        2500        2510        2520
CNTCTAGCAT ATAGACTATA TAATCAGATT GACAGCATAT AGAATATATT ATCAGACAAG ATGAGGAGGT
      2530        2540        2550        2560        2570        2580        2590
ACAAAAGTTA CTATTGCTCA TAATGACTTA CAGGCTAAAA NTAGNTNTAA AATACTATAT TAAATTCTGA
      2600        2610        2620        2630        2640        2650        2660
ATGCAATTTT TTTTTGTTCC CTTGAGACCA AAATTTAAGT TAACTGTTGC TGGCAGTCTA AGTGTAAATG
      2670        2680        2690        2700        2710        2720        2730
TTAACAGCAG GAGAAGTTAA GAATTGAGCA GTTCTGTTGC ATGATTTCCC AAATGAAATA CTGCCTTGGC
      2740        2750        2760        2770        2780        2790        2800
TAGAGTTTGA AAAACTAATT GAGCCTGTGC CTGGCTAGAA AACAAGCGTT TATTTGAATG TGAATAGTGT
      2810        2820        2830        2840        2850        2860        2870
TTCAAAGGTA TGTAGTTACA GAATTCCTAC CAAACAGCTT AAATTCTTCA AGAAAGAATT CCTGCAGCAG
      2880        2890        2900        2910        2920        2930        2940
TTATTCCCTT ACCTGAAGGC TTCAATCATT TGGATCAACA ACTGCTACTC TCGGGAAGAC TCCTCTACTC
      2950        2960        2970        2980        2990        3000        3010
ACAGCTGAAG AAAATGAGCA CACCCTTCAC ACTGTTATCA CCTATCCTGA AGATGTGATA CACTGAATGG
      3020        3030        3040        3050        3060        3070        3080
AAATAAATAG ATGTAAATAA AATTGAGWTC TCATTTAAAA AAAACCATGT GCCCAATGGG AAAATGACCT
      3090        3100        3110        3120        3130        3140        3150
CATGTTGTGG TTTAAACAGC AACTGCACCC ACTAGCACAG CCCATTGAGC TANCCTATAT ATACATCTCT
      3160
GTCAGTGCCC CTC
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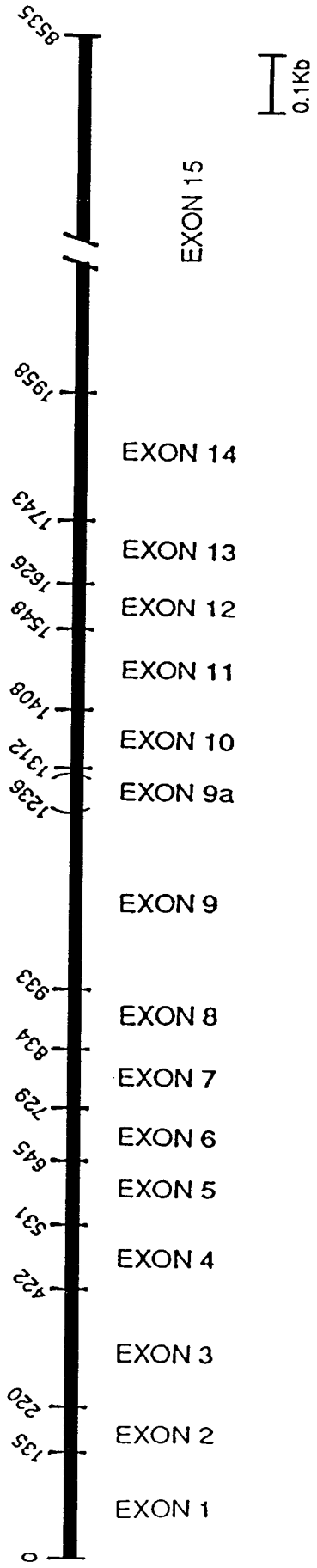

FIG. 7A

FIG. 7B-1

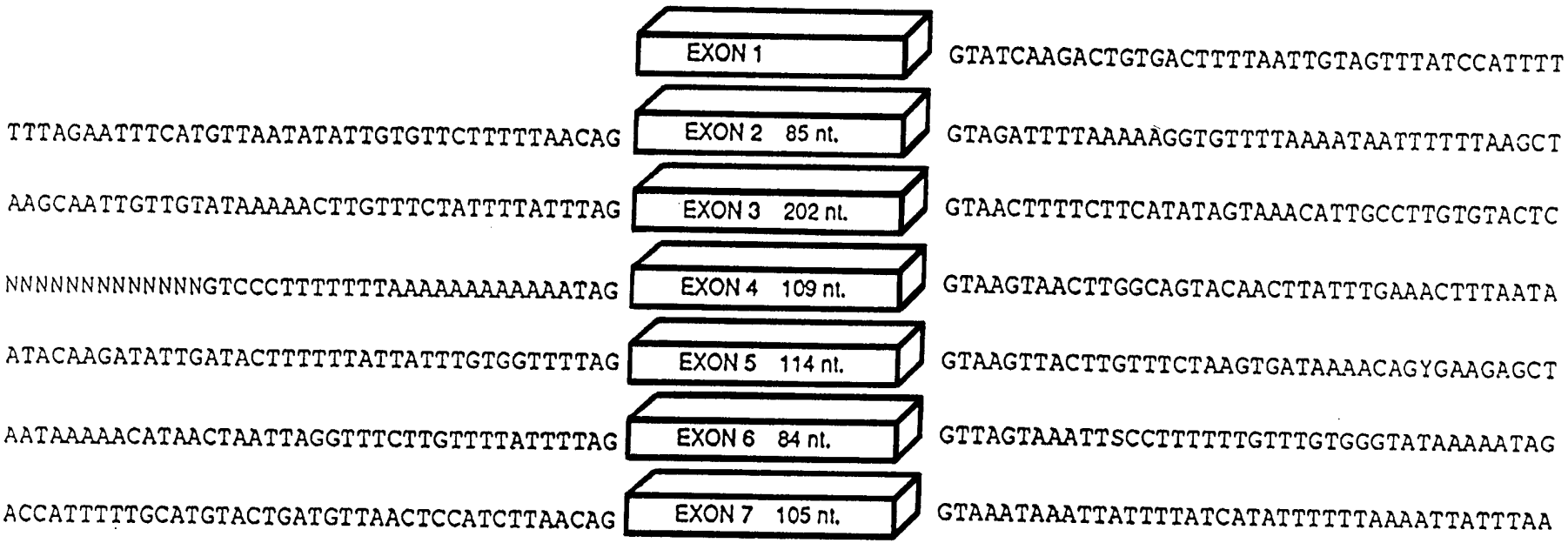

FIG. 7B-2